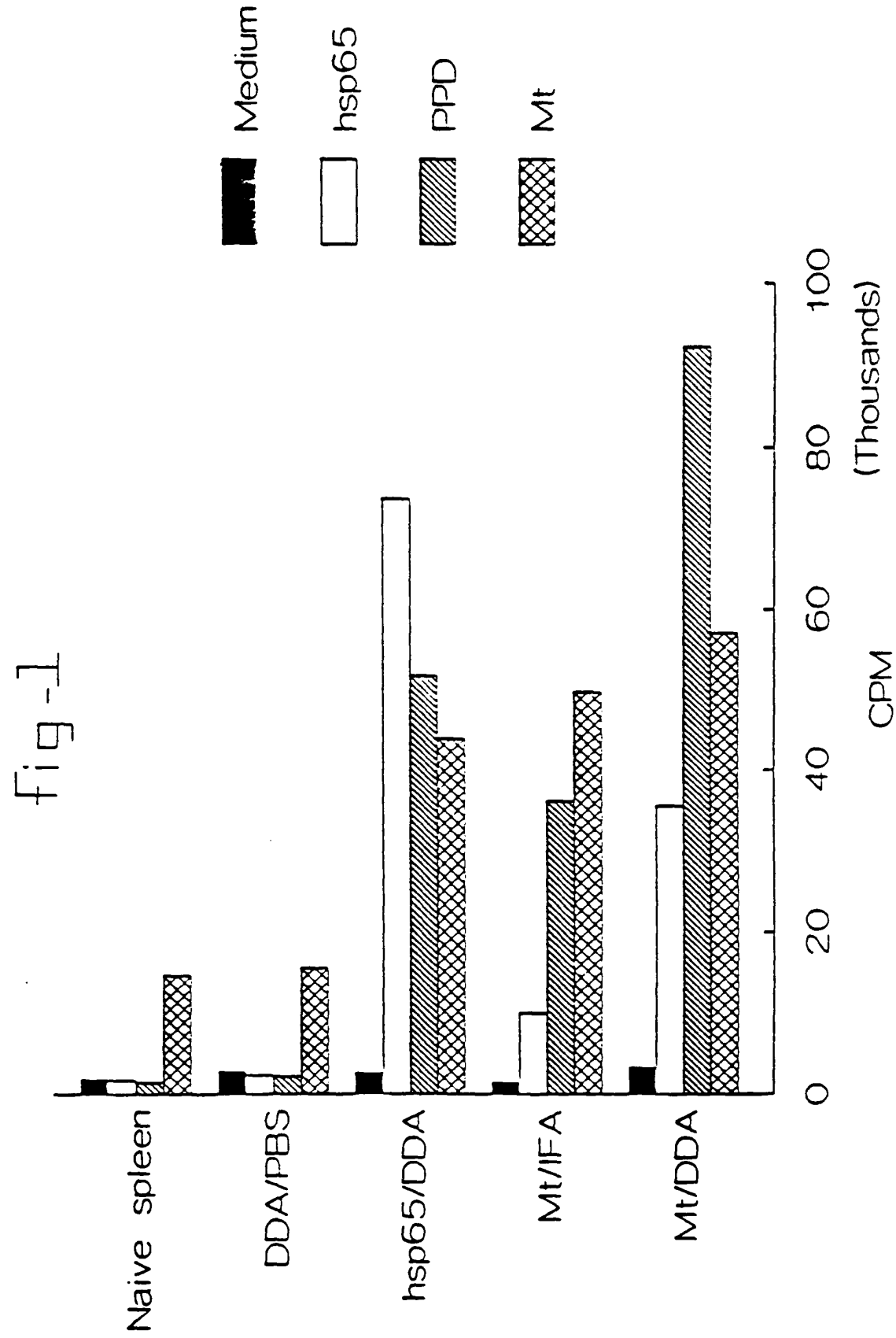

Medium
hsp65
PPD
Mt
Naive spleen
DDA/PBS
hsp65/DDA
Mt/IFA
Mt/DDA
0
20
40
60
80
100
CPM
(Thousands)

fig-1

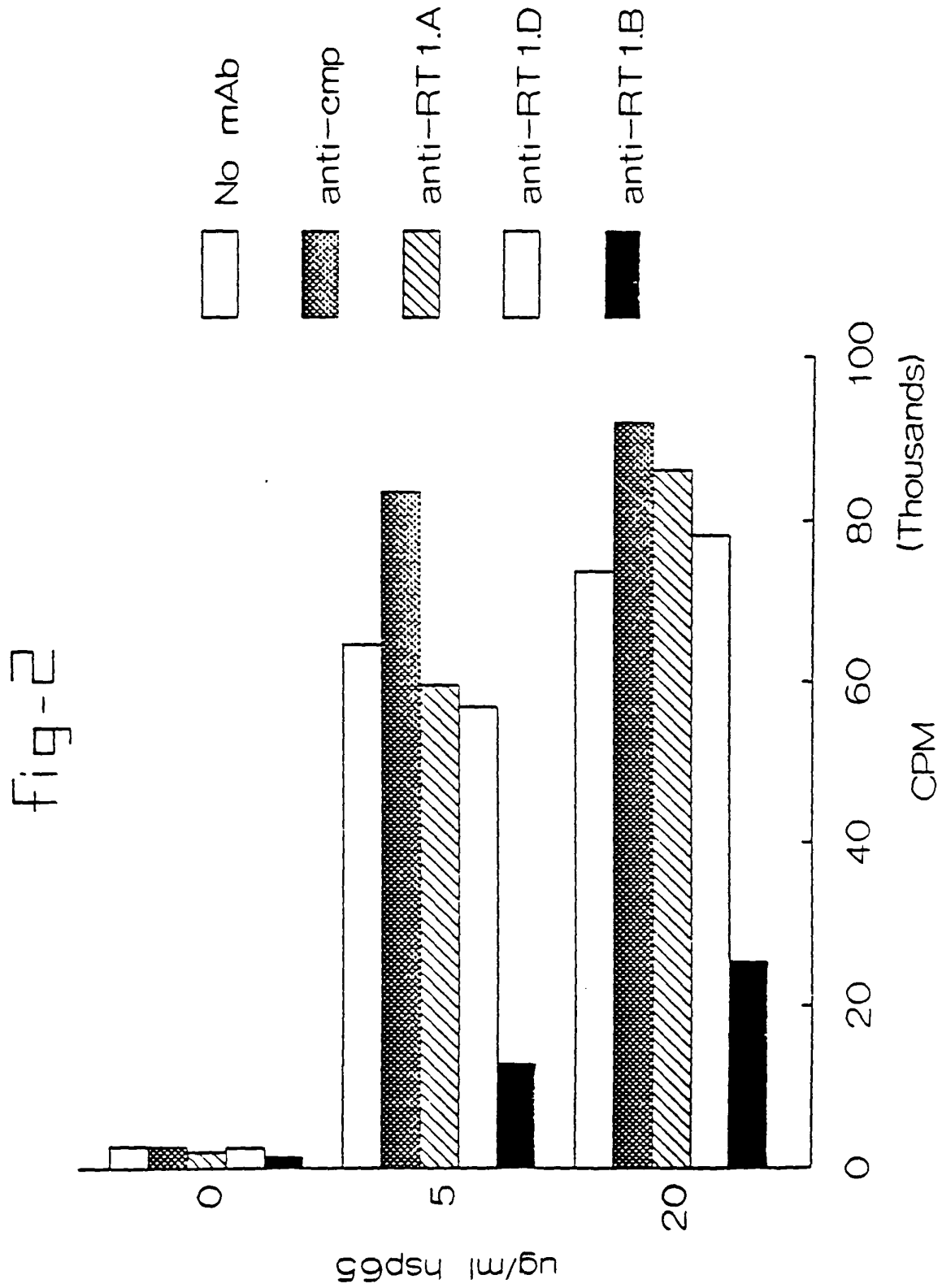

No mAb
anti-cmp
anti-RT 1.A
anti-RT 1.D
anti-RT 1.B
0
20
40
60
80
100
(Thousands)
CPM
0
5
20
ug/ml hsp65

Fig-2

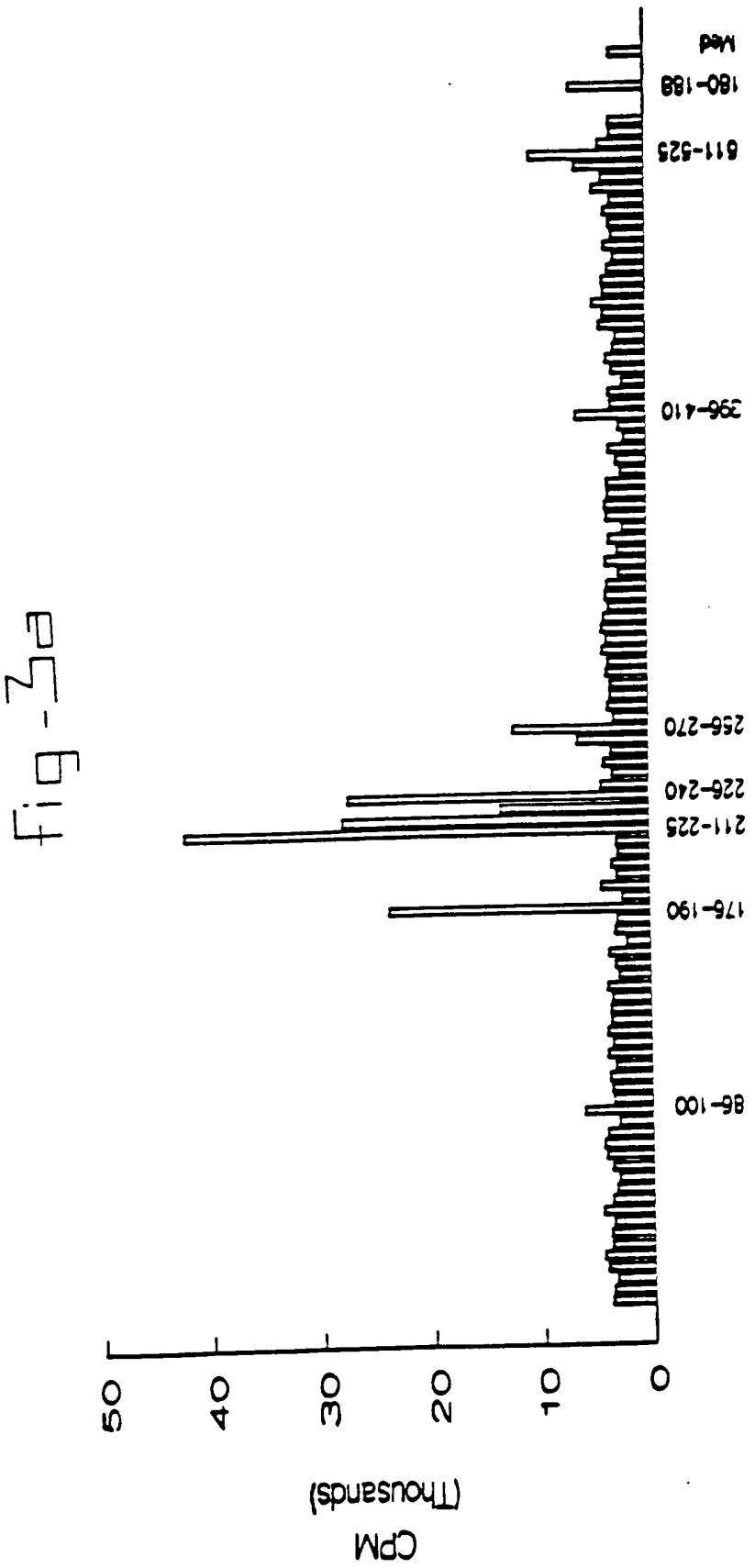

CPM
(Thousands)
50
40
30
20
10
0
86-100
176-190
211-225
226-240
256-270
296-410
811-825
180-188
Mkd

Fig-3a

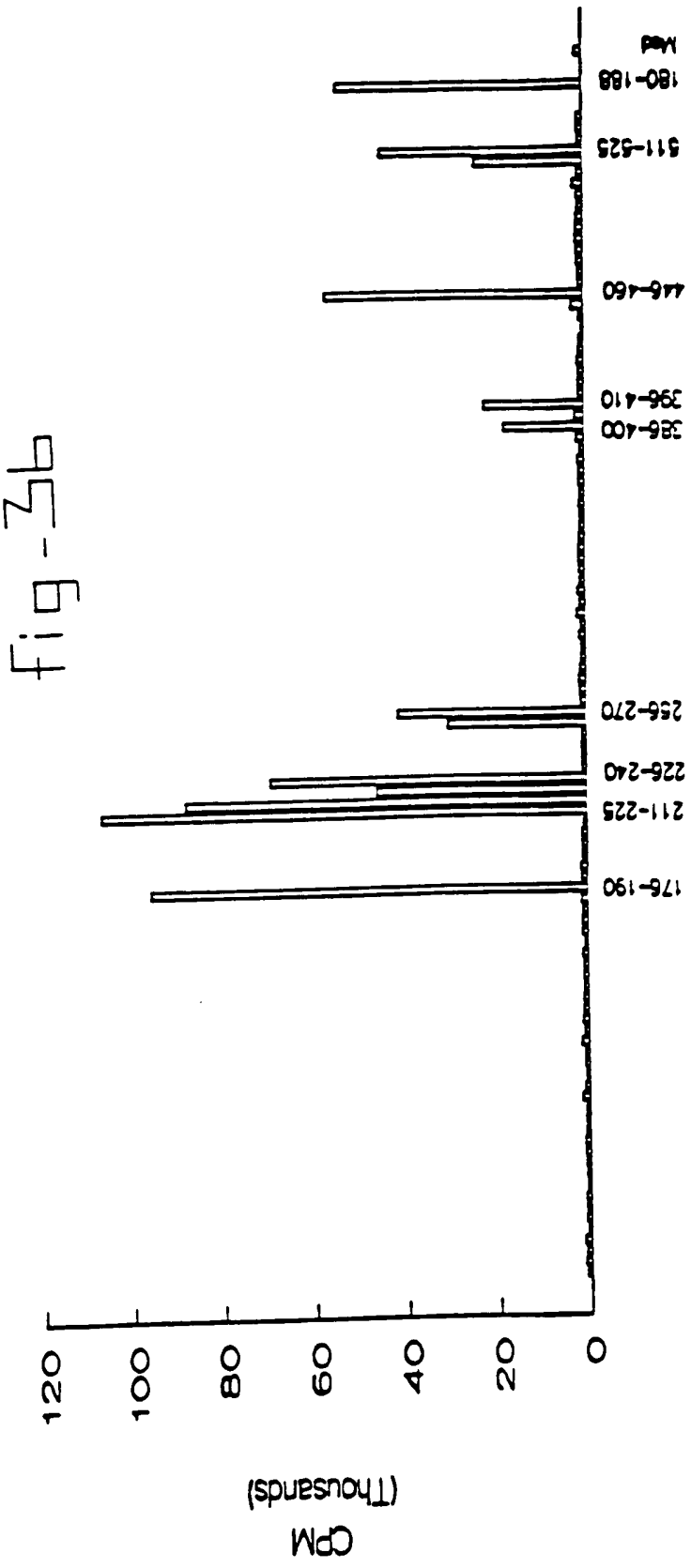

CPM
(Thousands)
0
20
40
60
80
100
120
176-190
211-225
226-240
256-270
386-400
396-410
446-460
511-525
180-188
Mkd

Fig-3b

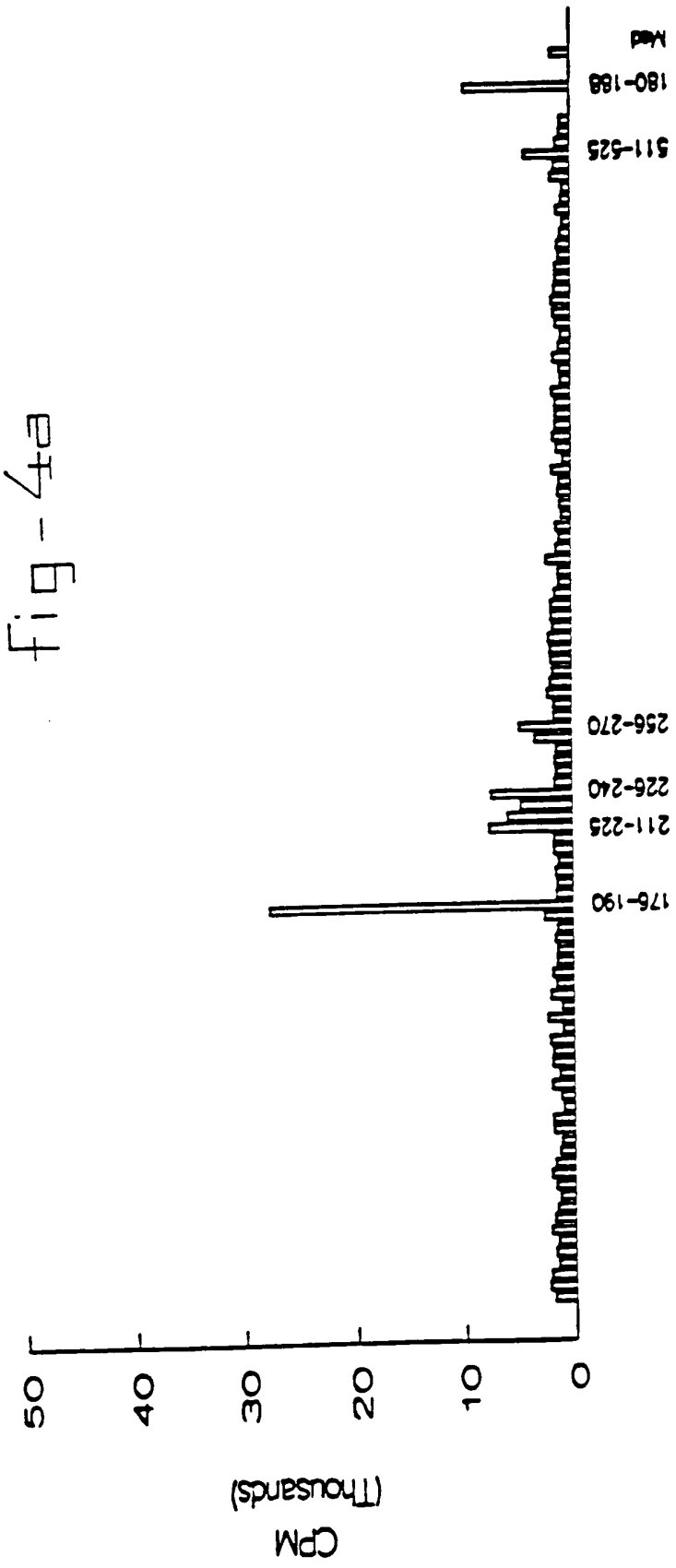

CPM
(Thousands)
0
10
20
30
40
50
176-190
211-225
226-240
256-270
511-525
180-188
Mrd

Fig - 4a

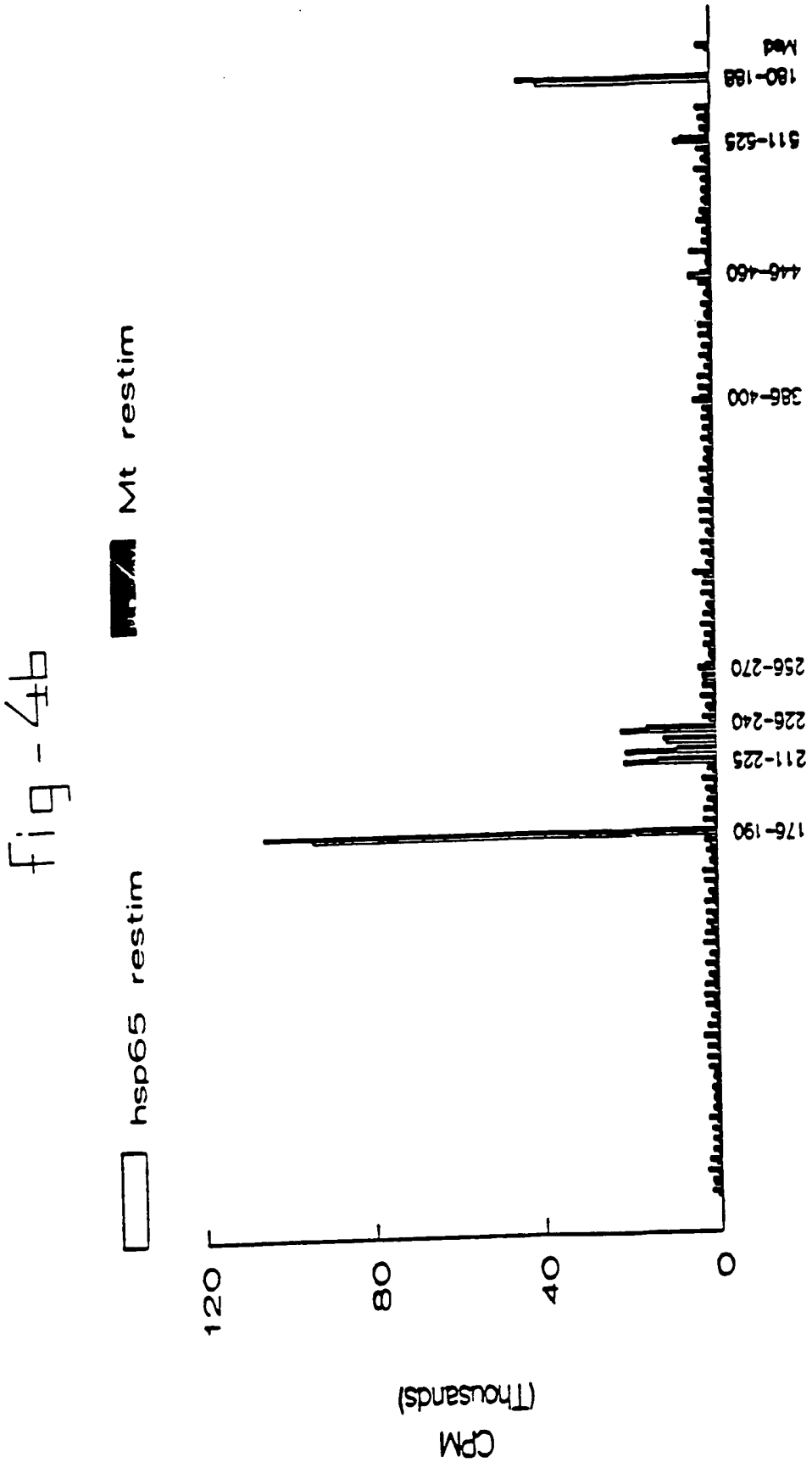

CPM
(Thousands)
120
80
40
0
hsp65 restim
Mt restim
176-190
211-225
226-240
256-270
386-400
446-460
511-525
180-188
Mad

Fig-4b

Fig - 5.1

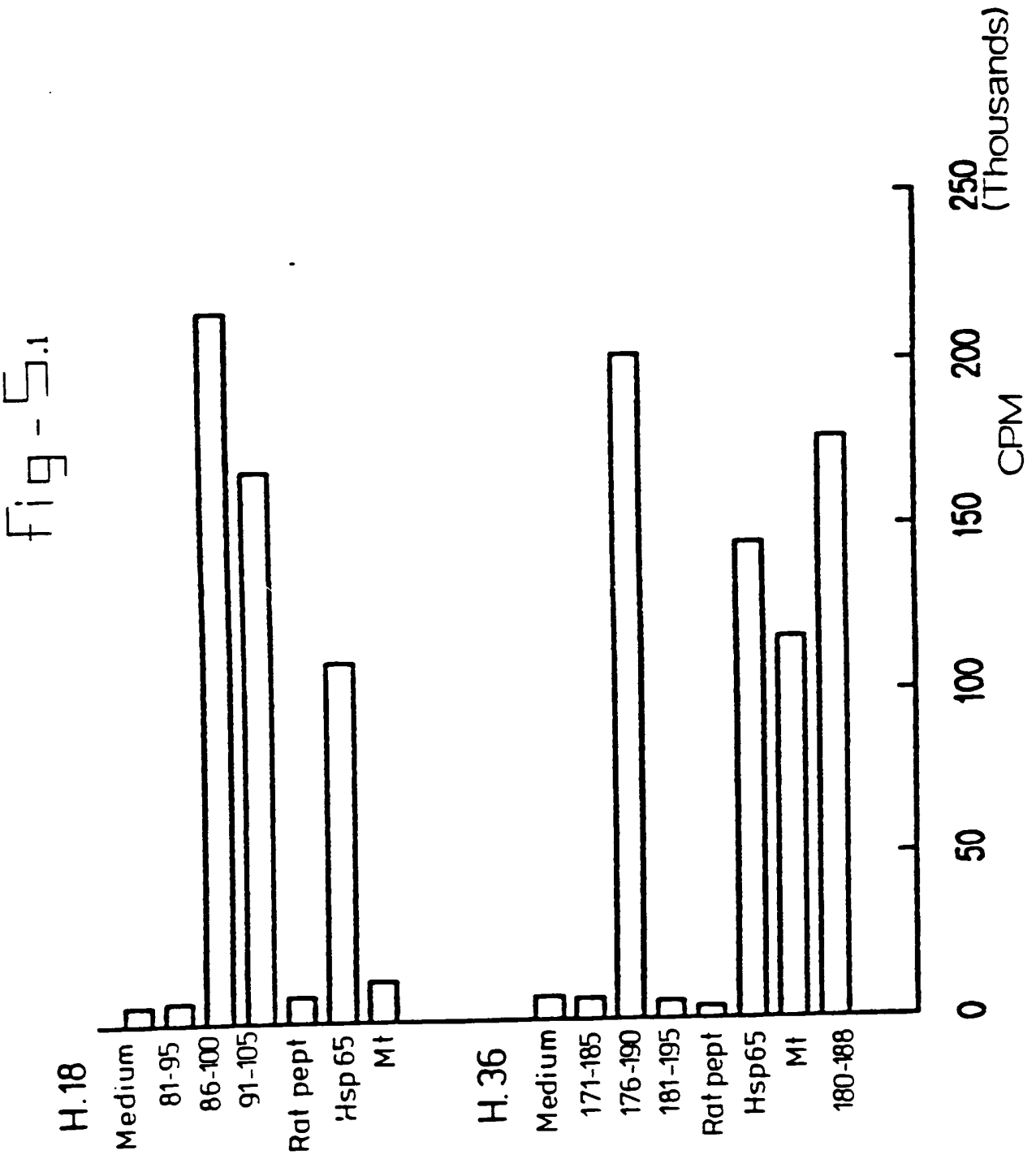

H.18
Medium
81-95
86-100
91-105
Rat pept
Hsp 65
Mt
H.36
Medium
171-185
176-190
181-195
Rat pept
Hsp65
Mt
180-188
0
50
100
150
200
250
CPM
(Thousands)

Fig - 5.2

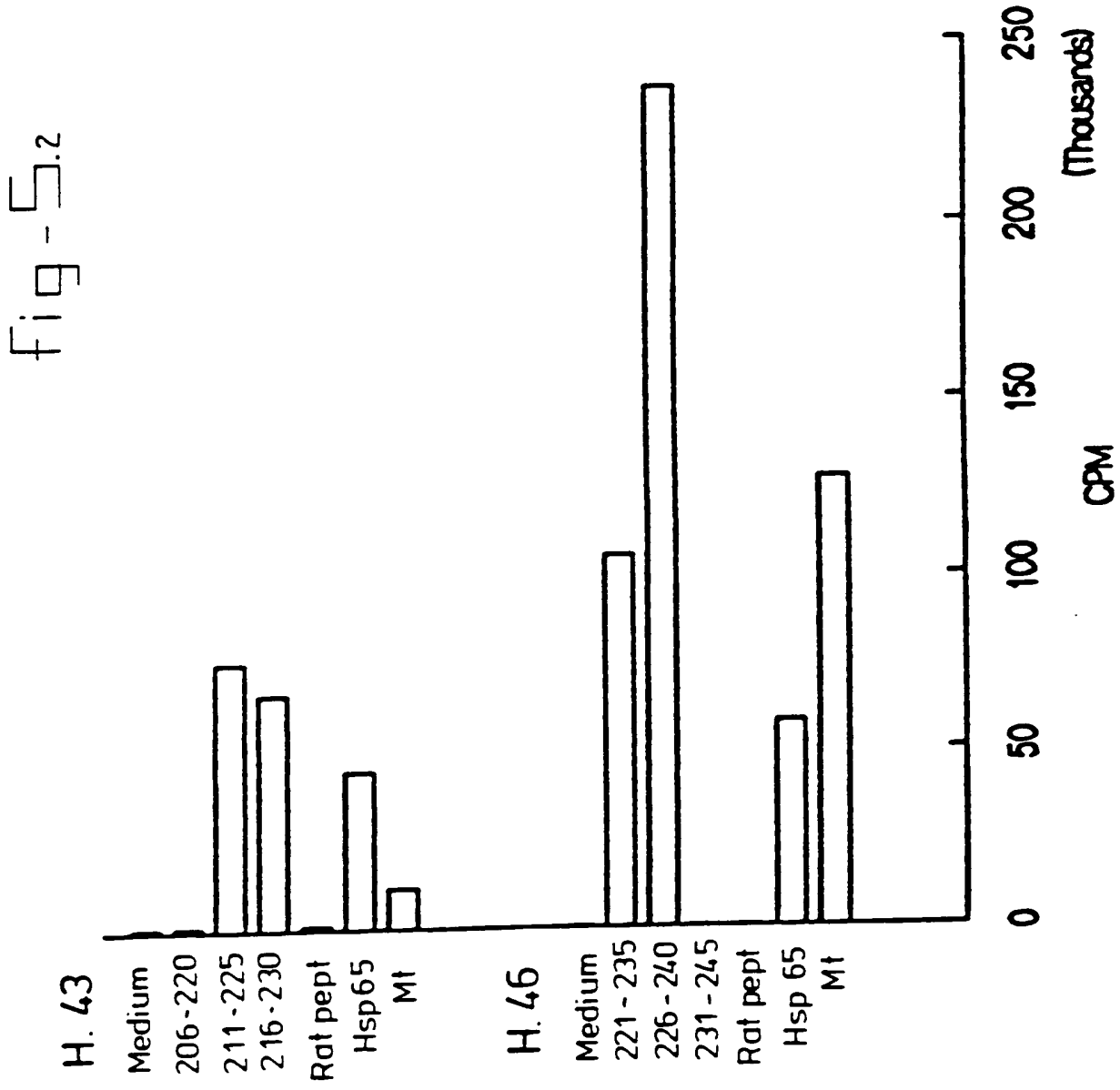

H. 43
Medium
206-220
211-225
216-230
Rat pept
Hsp65
Mt
H. 46
Medium
221-235
226-240
231-245
Rat pept
Hsp 65
Mt
0
50
100
150
200
250
(Thousands)
CPM

Fig - 5.3

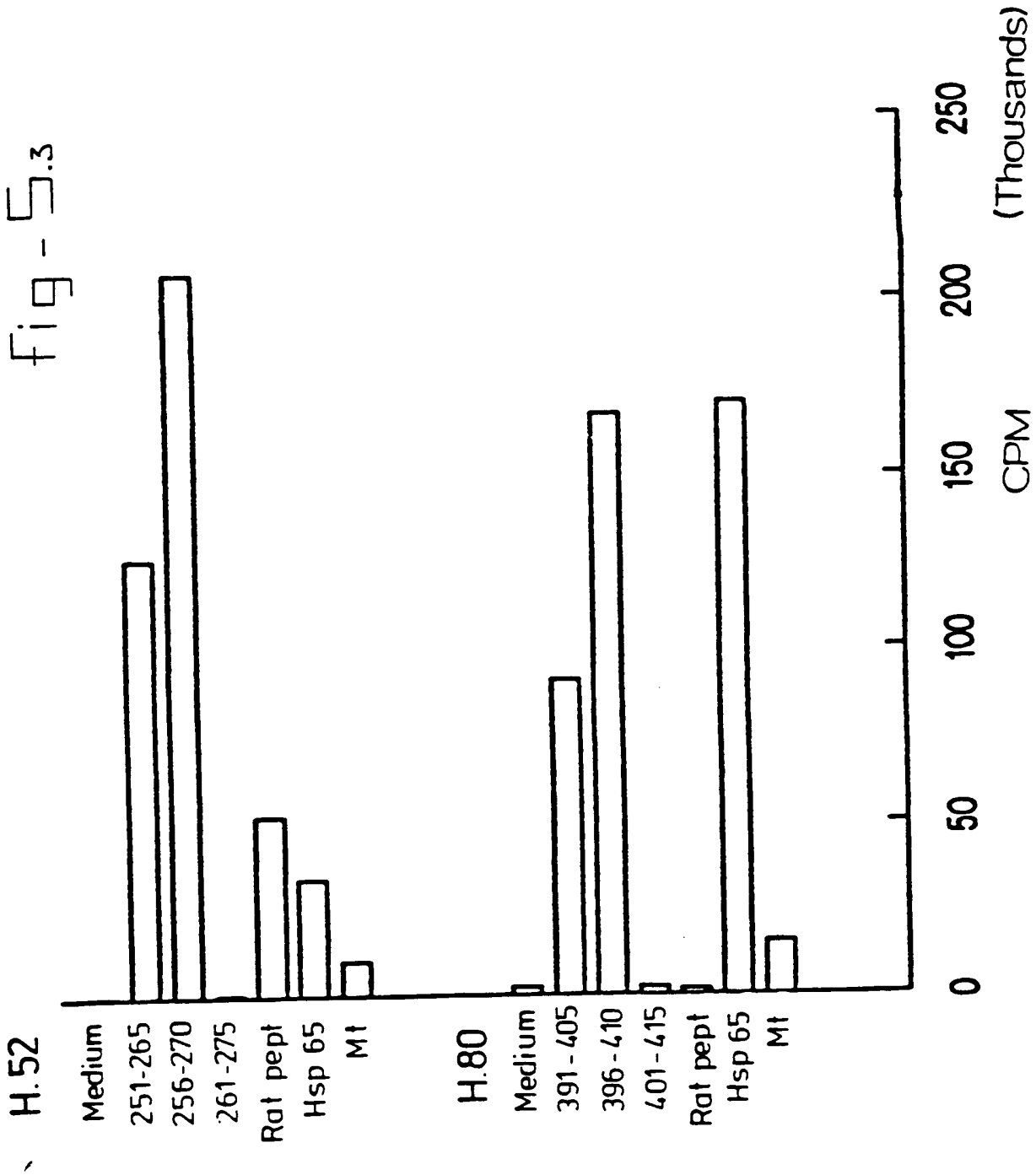

H.52
Medium
251-265
256-270
261-275
Rat pept
Hsp 65
Mt
H.80
Medium
391-405
396-410
401-415
Rat pept
Hsp 65
Mt
0
50
100
150
200
250
CPM
(Thousands)

Fig - 5.4

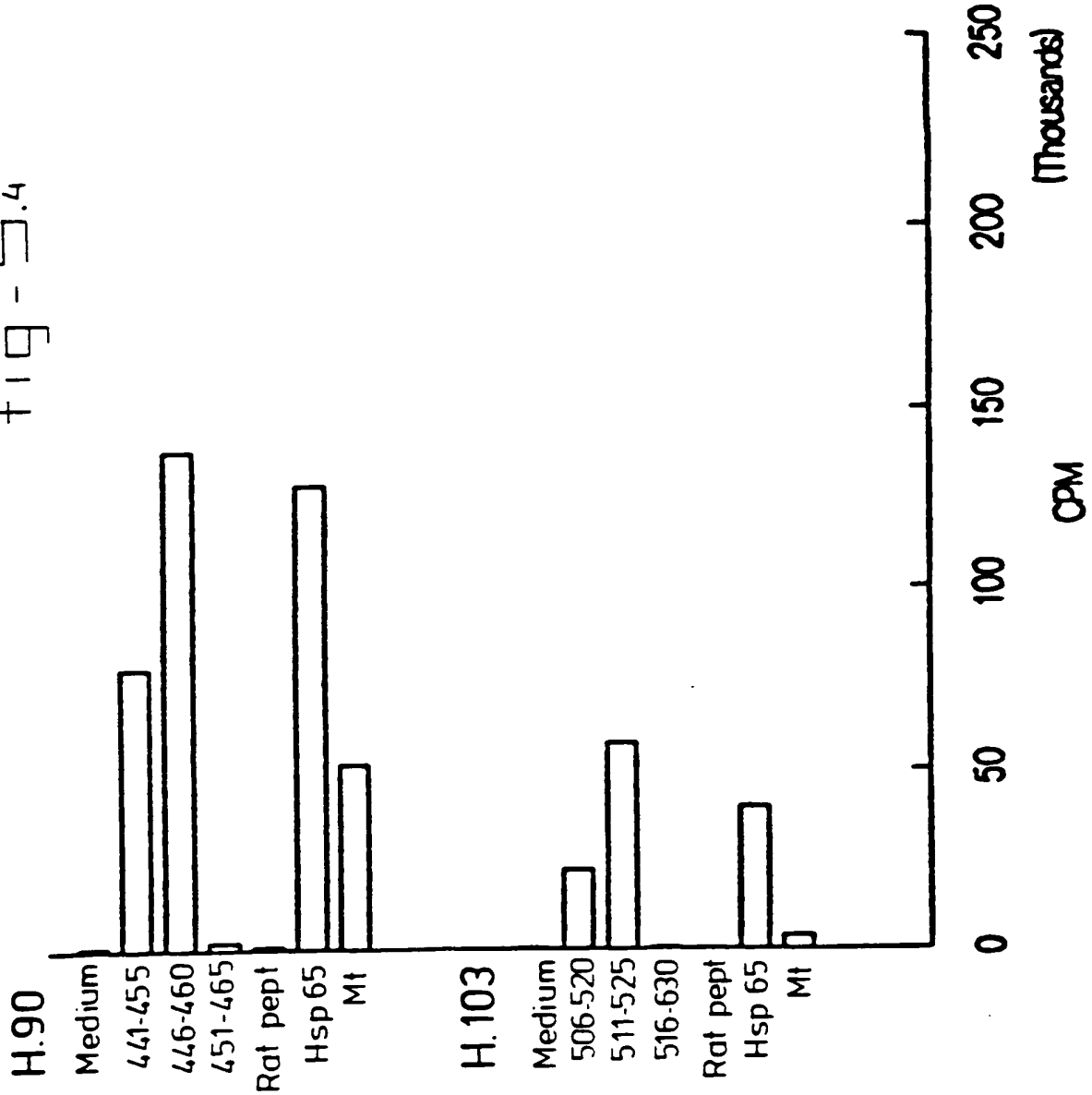
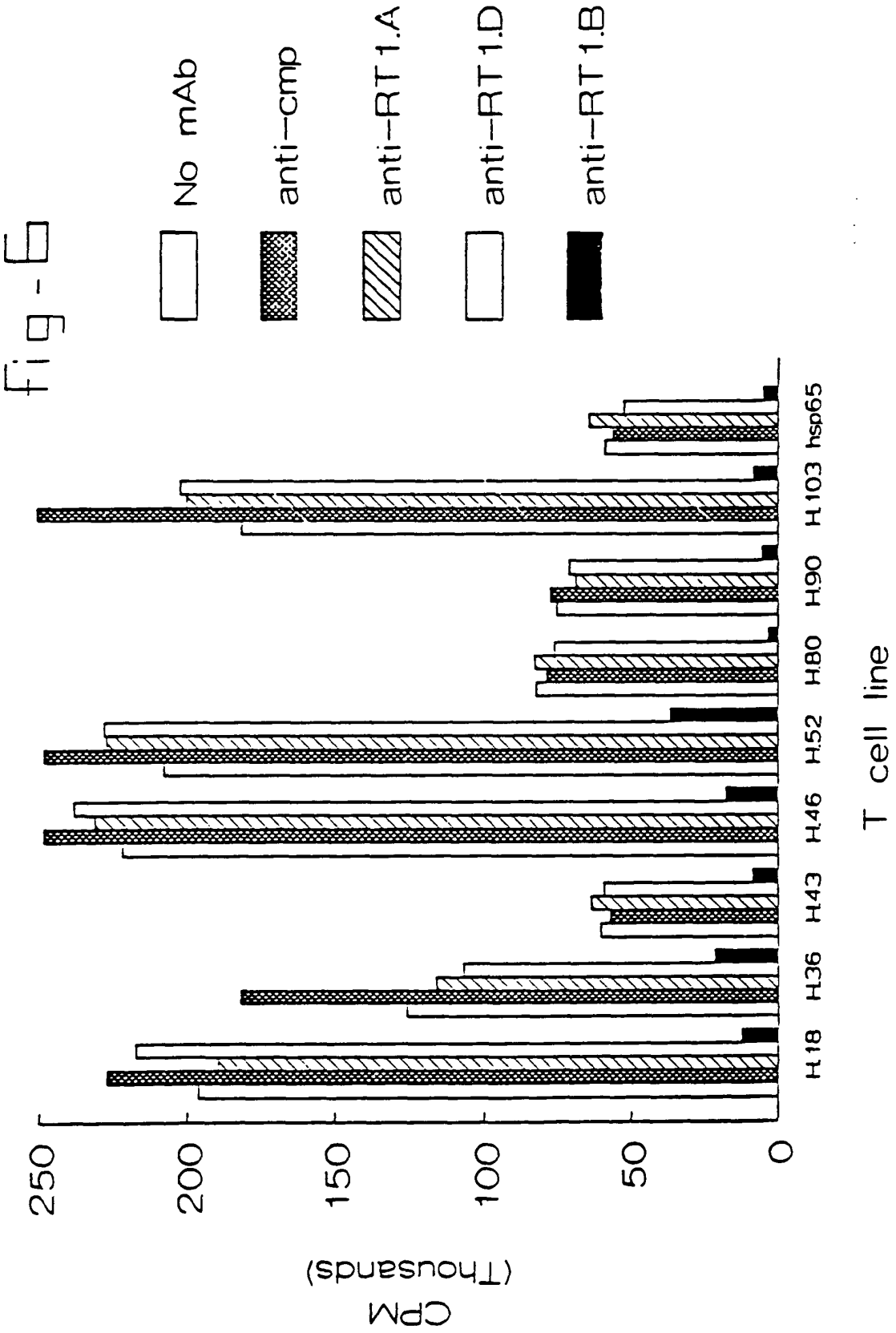

H.90
Medium
441-455
446-460
451-465
Rat pept
Hsp 65
Mt
H.103
Medium
506-520
511-525
516-630
Rat pept
Hsp 65
Mt
0
50
100
150
200
250
(Thousands)
CPM

Fig-6


No mAb
anti-cmp
anti-RT1.A
anti-RT1.D
anti-RT1.B
CPM
(Thousands)
250
200
150
100
50
0
H18
H36
H43
H46
H52
H80
H90
H103 hsp65
T cell line

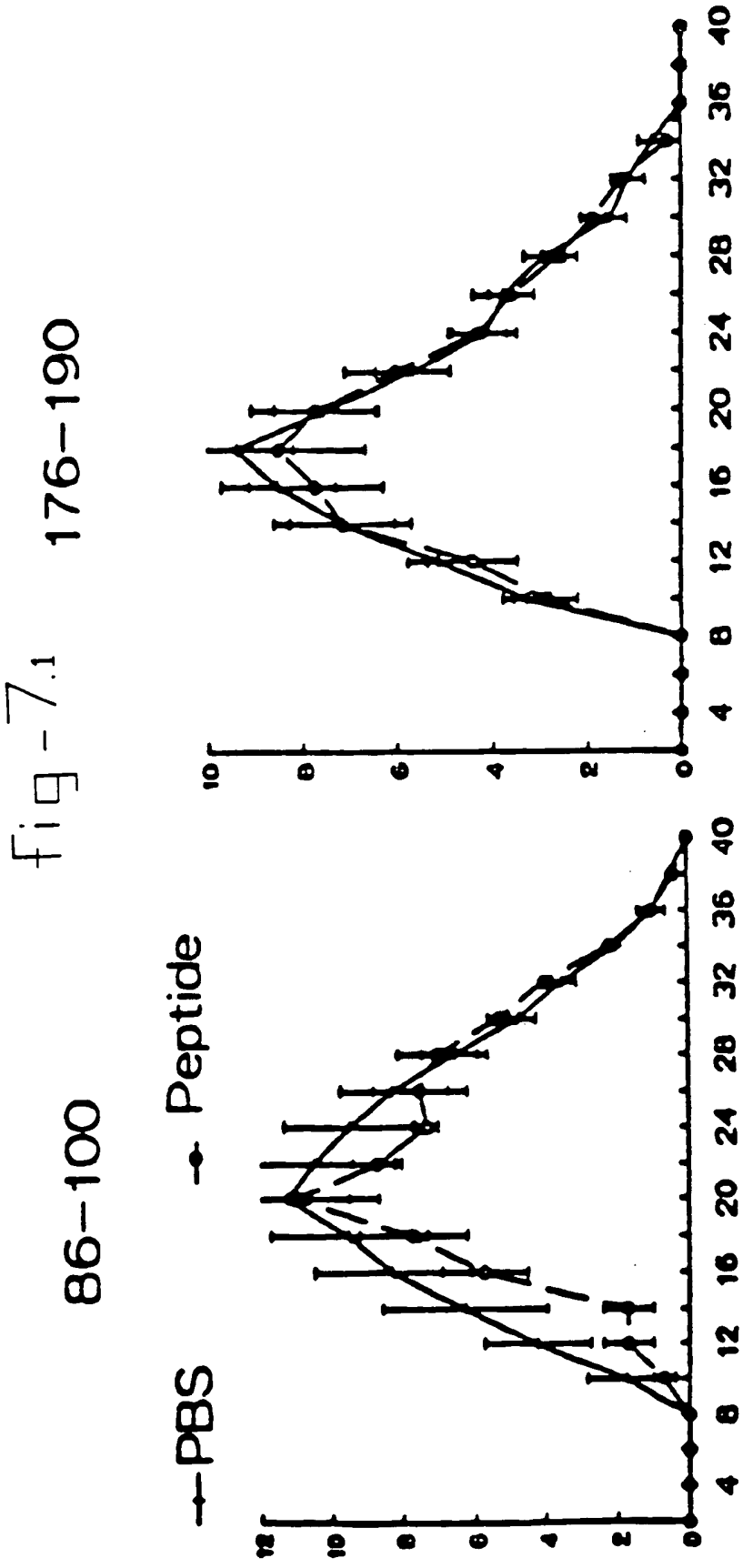


fig-7.1
86–100
176–190
PBS
Peptide
0
2
4
6
8
10
12
4
8
12
16
20
24
28
32
36
40

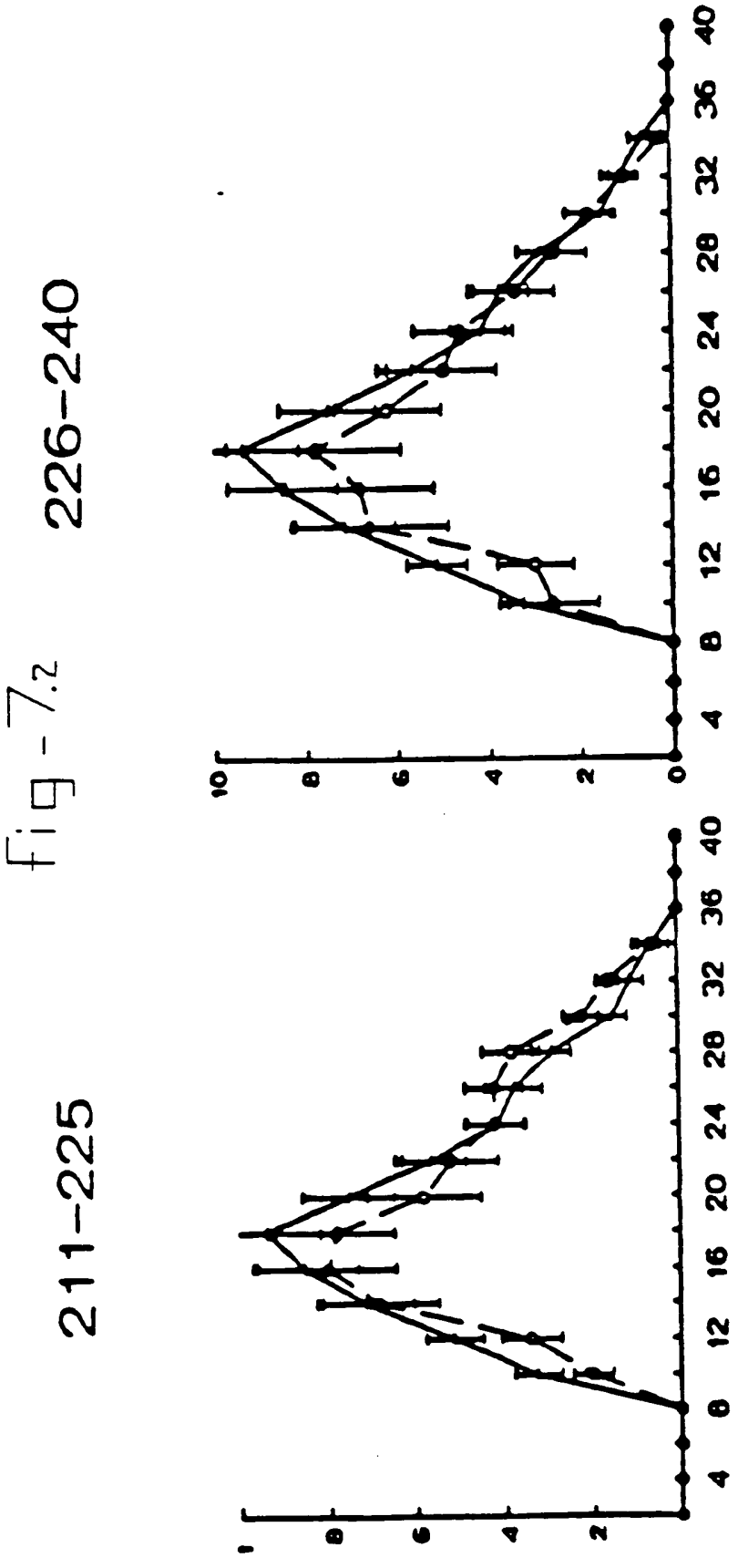



Fig - 7.2

Fig - 7.3

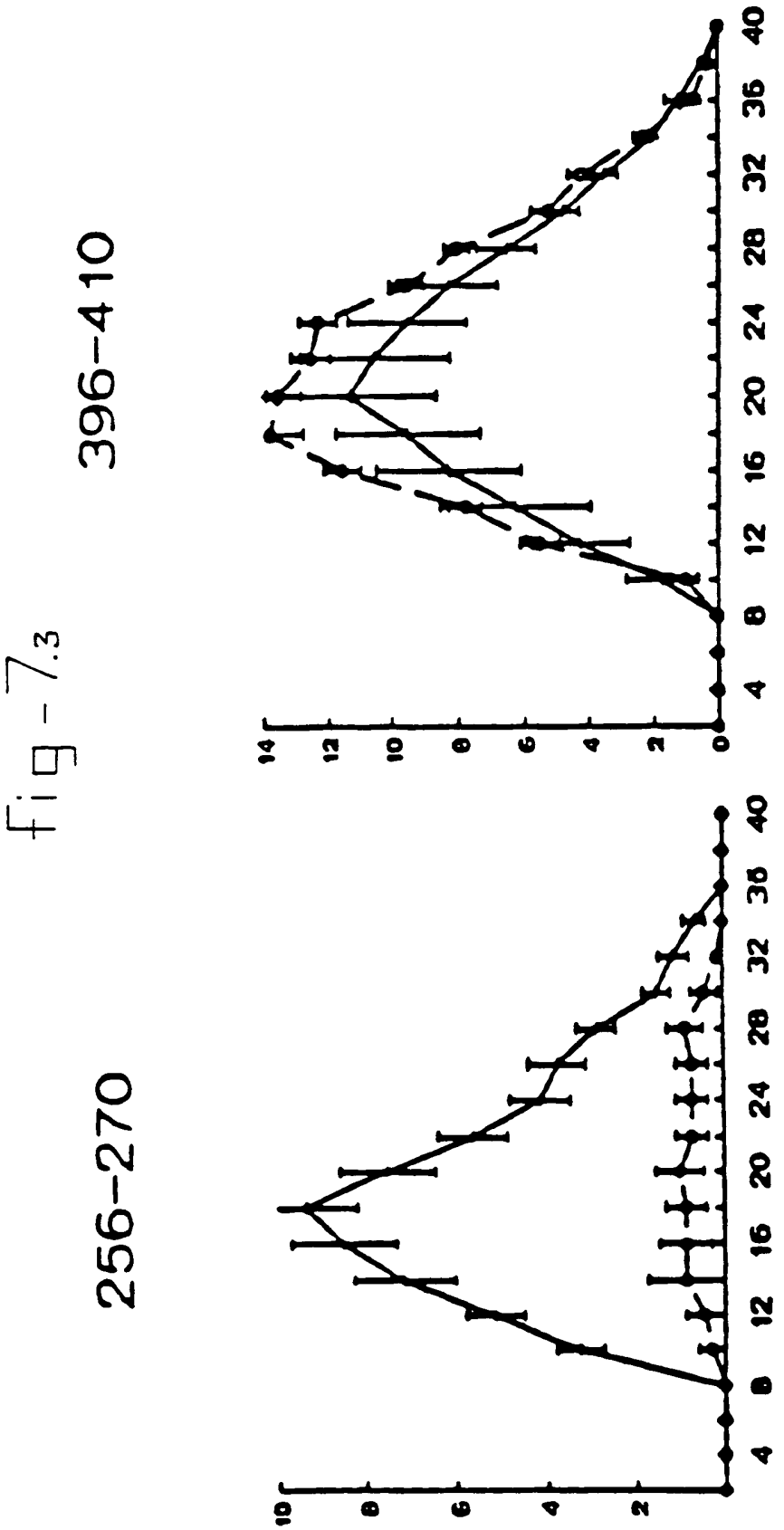
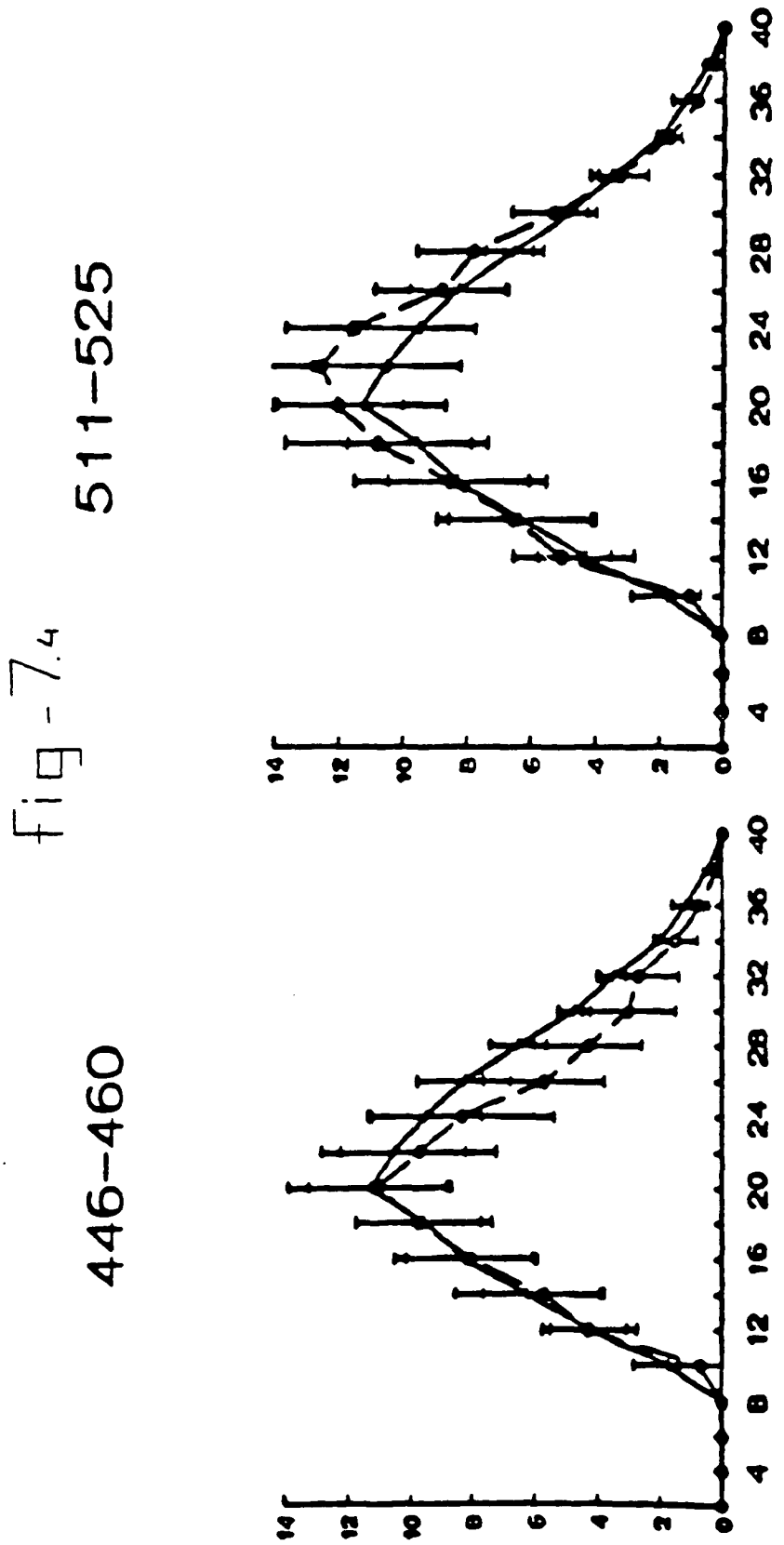


Fig - 7.4



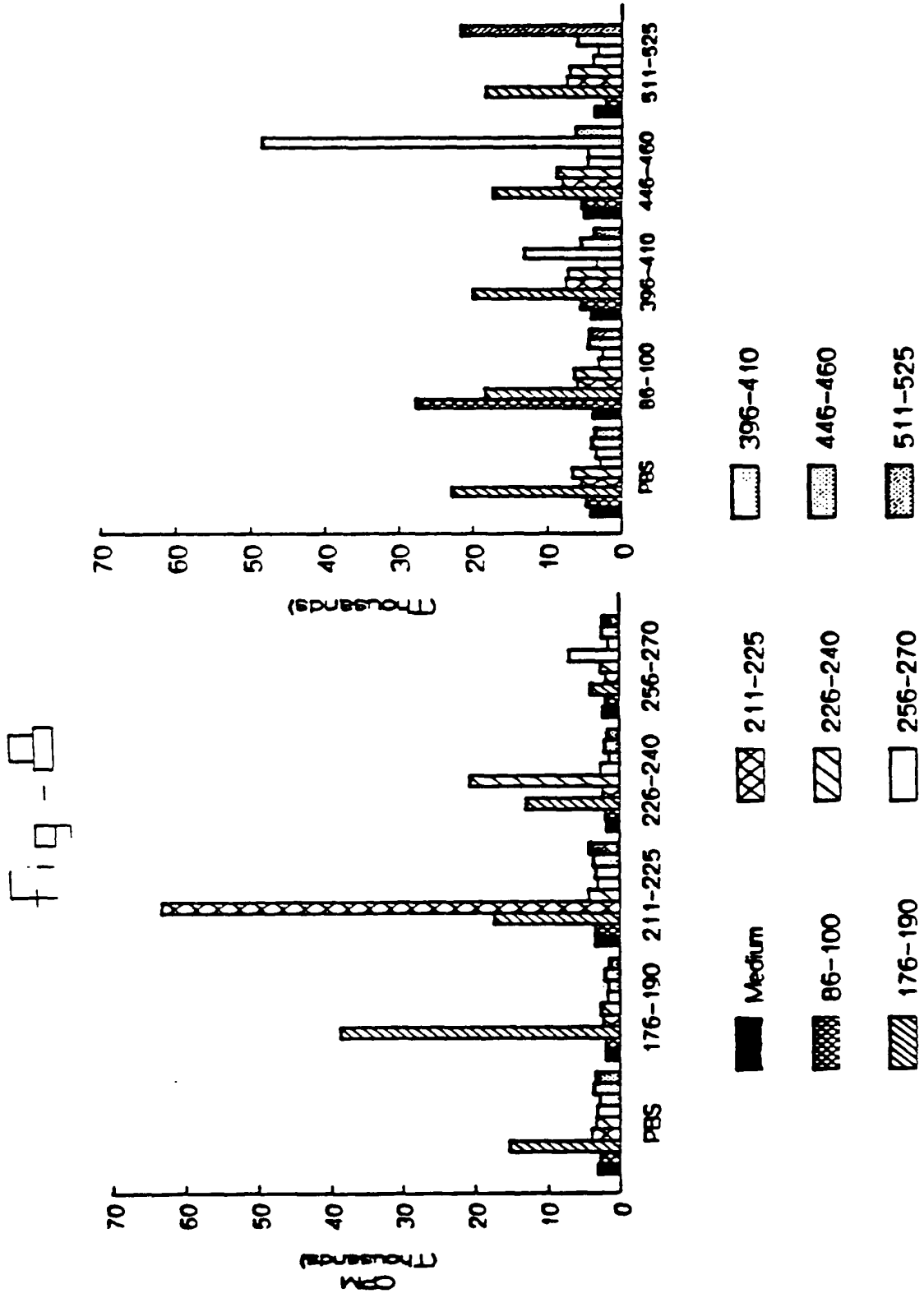


Fig - 6
Thousands
70
60
50
40
30
20
10
0
PBS
176-190
211-225
226-240
256-270
86-100
396-410
446-460
511-525
Medium
211-225
226-240
256-270
396-410
446-460
511-525
86-100
176-190

08/716169
PCT/NL95/00108

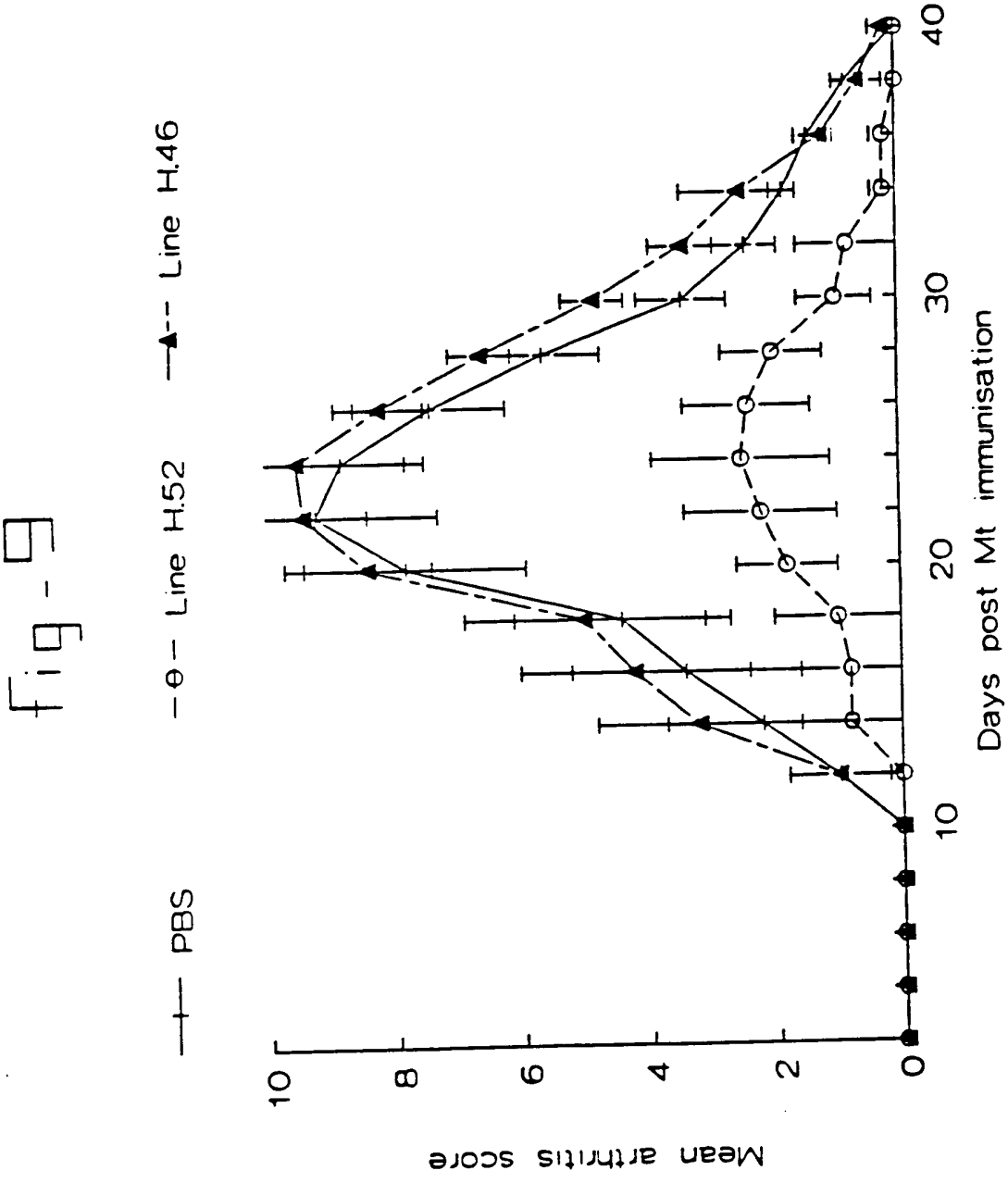
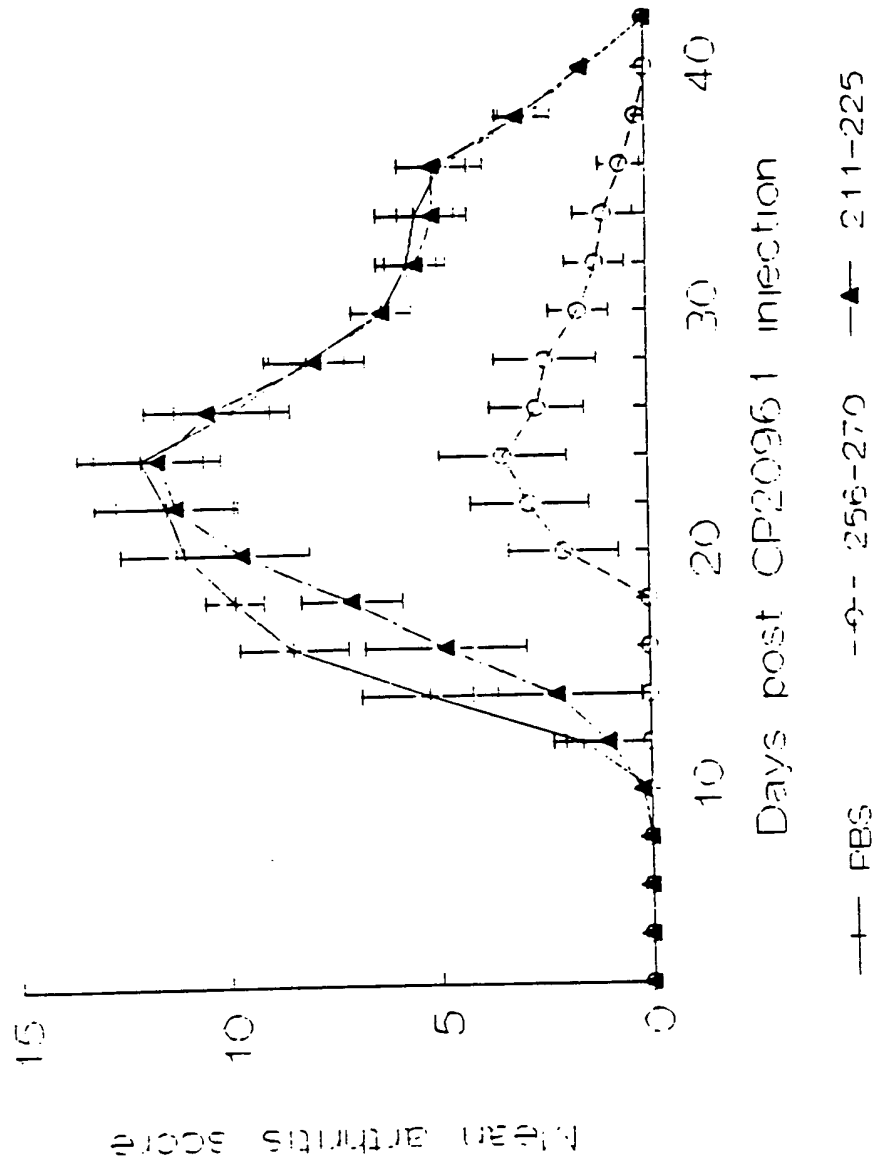



Fig - 5

Fig-10


Mean arthritis score
0
5
10
15
10
20
30
40
Days post CP20961 injection
FBS
256-270
211-225

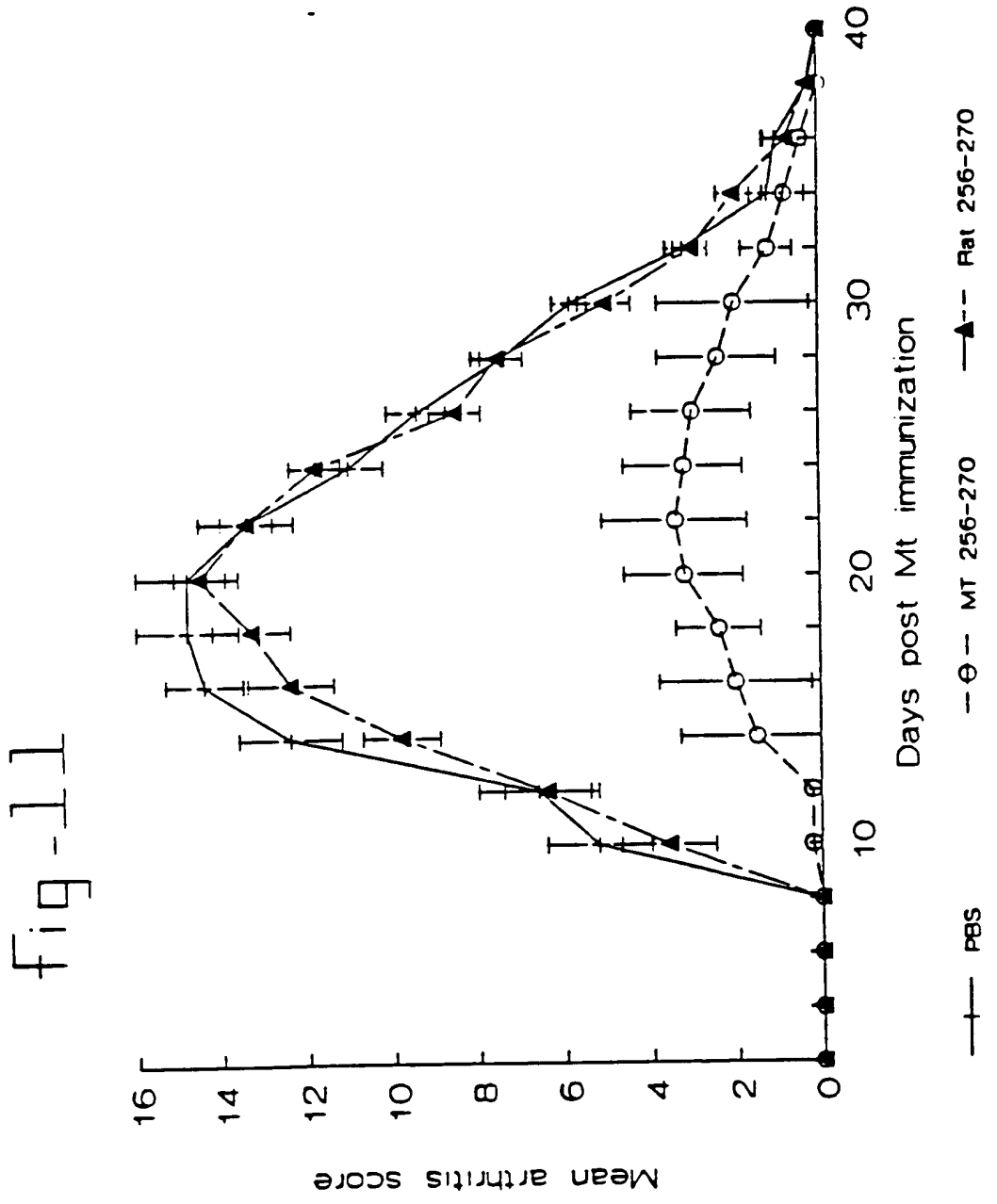
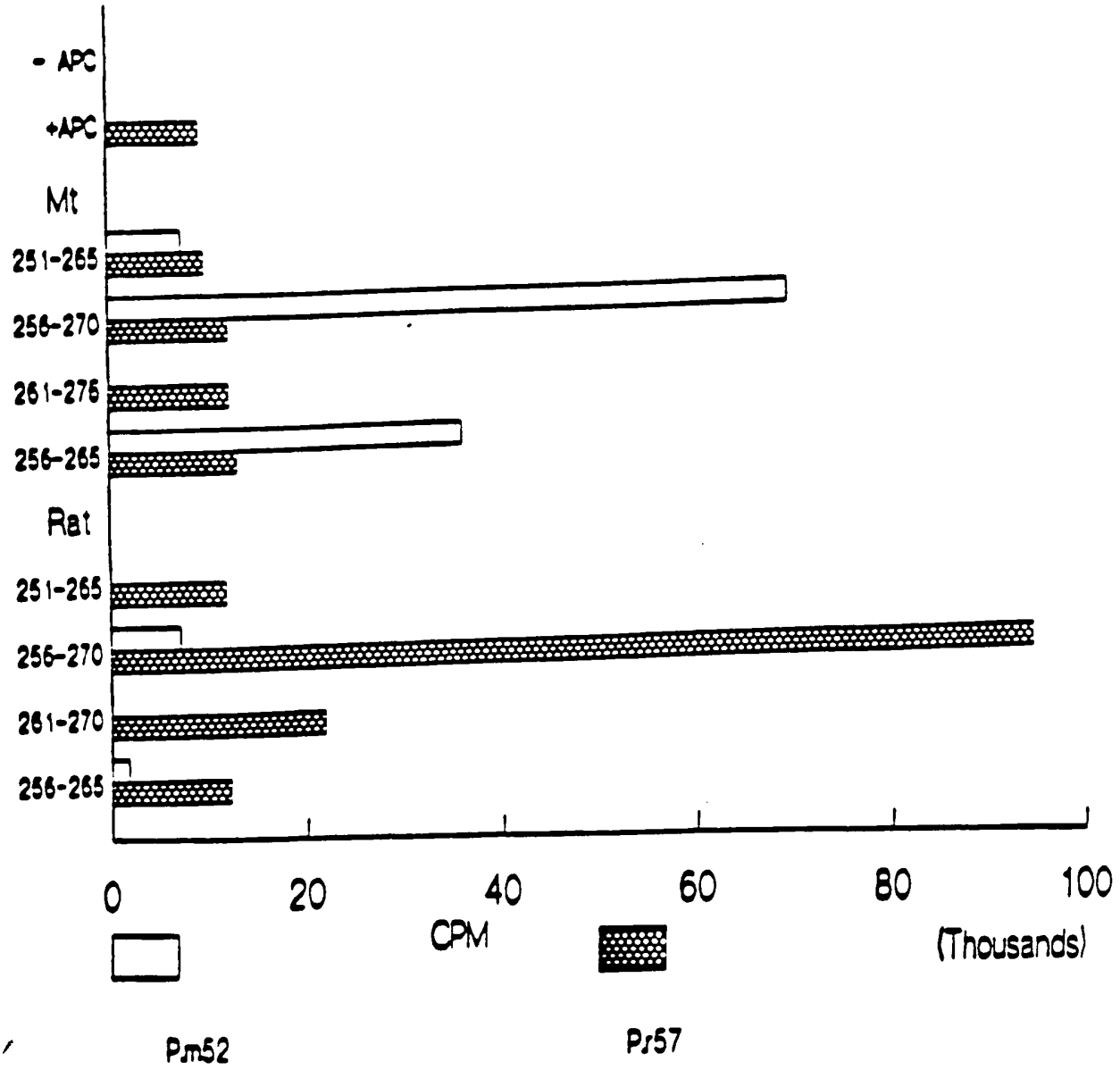

Mean arthritis score
0
2
4
6
8
10
12
14
16
10
20
30
40
Days post Mt immunization
PBS
MT 256-270
Rat 256-270

Fig-11

fig-12


- APC
+APC
Mt
251-265
256-270
261-276
256-265
Rat
251-265
256-270
261-270
256-265
0
20
40
60
80
100
CPM
(Thousands)
Pm52
Pr57

# Fig. 13 (1)

```
****************************************
* MULTIPLE SEQUENCE ALIGNMENT HSP60 *
****************************************

HUMAN   MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKF    32
RAT     ------------------A--------KDVKF     6
MOUSE   ------------------APHLTRAYAKDVKF    14
M.TUB   M-------------------------AKTIAY     7
                                   *.. .

HUMAN   GADARALMLQGVDLLADAVAVTMGPKGRTVII    64
RAT     GADARALMLQGVDLLADAVAVTMGPKGRTVII    38
MOUSE   GADARALMLQGVDLLADAVAVTMGPKGRTVII    46
M.TUB   DEEARRGLERGLNALADAVKVTLGPKGRNVVL    39
        ...**  . .*.. ***** **.*****.*..

HUMAN   EQSWGSPKVTKDGVTVAKSIDLKDKYKNIGAK    96
RAT     EQSWGSPKVTKDGVTVAKSIDLKDKYKNIGAK    70
MOUSE   EQSWGSPKVTKDGVTVAKSIDLKDKYKNIGAK    78
M.TUB   EKKWGAPTITNDGVSIAKEIELEDPYEKIGAE    71
        *..**.*..*.***..**.*.*.* *..***.

HUMAN   LVQDVANNTNEEAGDGTTTATVLARSIAKEGF   128
RAT     LVQDVANNTNEEAGDGTTTATVLARSIAKEGF   102
MOUSE   LVQDVANNTNEEAGDGTTTATVLARSIAKEGF   110
M.TUB   LVKEVAKKTDDVAGDGTTTATVLAQALVREGL   103
        **..**..*.. ************.....**.

HUMAN   EKISKGANPVEIRRGVMLAVDAVIAELKKQSK   160
RAT     EKISKGANPVEIRRGVMLAVDAVIAELKKQSK   134
MOUSE   EKISKGANPVEIRRGVMLAVDAVIAELKKQSK   142
M.TUB   RNVAAGANPLGLKRGIEKAVEKVTETLLKGAK   135
          ... ****....**.  **. *...* * .*

HUMAN   PVTTPEEIAQVATISANGDKEIGNIISDAMKK   192
RAT     PVTTPEEIAQVATISANGDKDIGNIISDAMKK   166
MOUSE   PVTTPEEIAQVATISANGDKDIGNIISDAMKK   174
M.TUB   EVETKEQIAATAAISA-GDQSIGDLIAEAMDK   166
         *.* *.**..*.*** **..**..*..**.*

HUMAN   VGRKGVITVKDGKTLNDELEIIEGMKFDRGYI   224
RAT     VGRKGVITVKDGKTLNDELEIIEGMKFDRGYI   198
MOUSE   VGRKGVITVKDGKTLNDELEIIEGMKFDRGYI   206
M.TUB   VGNEGVITVEESNTFGLQLELTEGMRFDKGYI   198
        **..*****....*.. .**..***.**.***

HUMAN   SPYFINTSKGQKCEFQDAYVLLSEKKISSIQS   256
RAT     SPYFINTSKGQKCEFQDAYVLLSEKKISSVQS   230
MOUSE   SPYFINTSKGQKCEFQDAYVLLSEKKFSSVQS   238
M.TUB   SGYFVTDPERQEAVLEDPYILLVSSKVSTVKD   230
        * **..... *.  ..*.*.** ..* *....

HUMAN   IVPALEIANAHRKPLVIIAEDVDGEALSTLVL   288
RAT     IVPALEIANAHRKPLVIIAEDVDGEALSTLVL   262
MOUSE   IVPALEIANAHRKPLVIIAEDVDGEALSTLVL   270
M.TUB   LLPLLEKVIGAGKPLLIIAEDVEGEALSTLVV   262
        ..* ** . .  ***.******.********.
```

# Fig. 13 (2)

```
HUMAN   NRLKVGLQVVAVKAPGFGDNRKNQLKDMAIAT   320
RAT     NRLKVGLQVVAVKAPGFGDNRKNQLKDMAIAT   294
MOUSE   NRLKVGLQVVAVKAPGFGDNRKNQLKDMAIAT   302
M.TUB   NKIRGTFKSVAVKAPGFGDRRKAMLQDMAILT   294
        *... ... **********.**. *.**** *

HUMAN   GGAVFGEEGLTLNLEDVQPHDLGKVGEVIVTK   352
RAT     GGAVFGEEGLNLNLEDVQAHDLGKVGEVIVTK   326
MOUSE   GGAVFGEEGLNLNLEDVQAHDLGKVGEVIVTK   334
M.TUB   GGQVISEE-VGLTLENADLSLLGKARKVVVTK   325
        **.*..** ..*.**...   ***. .*.***

HUMAN   DDAMLLKGKGDKAQIEKRIQEIIEQLDVTTSE   384
RAT     DDAMLLKGKGDKAHIEKRIQEITEQLDITTSE   358
MOUSE   DDAMLLKGKGDKAHIEKRIQEITEQLDITTSE   366
M.TUB   DETTIVEGAGDTDAIAGRVAQIRQEIENSDSD   357
        *.. ...* **.. *. *...* .... ..*.

HUMAN   YEKEKLNERLAKLSDGVAVLKVGGTSDVEVNE   416
RAT     YEKEKLNERLAKLSDGVAVLKVGGTSDVEVNE   390
MOUSE   YEKEKLNERLAKLSDGVAVLKVGGTSDVEVNE   398
M.TUB   YDREKLQERLAKLAGGVAVIKAGAATEVELKE   389
        *..***.******..****.*.*....**..*

HUMAN   KKDRVTDALNATRAAVEEGIVLGGGCALLRCI   448
RAT     KKDRVTDALNATRAAVEEGIVLGGGCALLRCI   422
MOUSE   KKDRVTDALNATRAAVEEGIVLGGGCALLRCI   430
M.TUB   RKHRIEDAVRNAKAAVEEGIVAGGGVTLLQAA   421
        .*.*..**.....******** *** .**.

HUMAN   PALDSLTPANEDQKIGIEIIKRTLKIPAMTIA   480
RAT     PALDSLKPANEDQKIGIEIIKRALKIPAMTIA   454
MOUSE   PALDSLKPANEDQKIGIEIIKRALKIPAMTIA   462
M.TUB   PTLDELK-LEGDEATGANIVKVALEAPLKQIA   452
        *.**.*.  ..*. .* .*.* .*. * . **

HUMAN   KNAGVEGSLIVEKIMQSSSEVGYDAMAGDFVN   512
RAT     KNAGVEGSLIVEKILQSSSEVGYDAMLGDFVN   486
MOUSE   KNAGVEGSLIVEKILQSSSEVGYDAMLGDFVN   494
M.TUB   FNSGLEPGVVAEKVRNLPAGHGLNAQTGVYED   484
         *.*.* ....**. . ... * .*  * . .

HUMAN   MVEKGIIDPTKVVRTALLDAAGVASLLTTAEV   544
RAT     MVEKGIIDPTKVVRTALLDAAGVASLLTTAEA   518
MOUSE   MVEKGIIDPTKVVRTALLDAAGVASLLTTAEA   526
M.TUB   LLAAGVADPVKVTRSALQNAASIAGLFLTTEA   516
        ... *. **.**.*.** .**..*.*. *.*.

HUMAN   VVTEIPKEEKDPGMGAMGGMGGGMGGGMF   573
RAT     VVTEIPKEEKDPGMGAMGGMGGGMGGGMF   547
MOUSE   VVTEIPKEEKDPGMGAMGGMGGGMGGGMF   555
M.TUB   VVADKPEKEKASVPG-----GGDMGGMDF   540
        **.. *..**..  *     **.***  *
```

Consensus 1 ngth: 573
Identity (*)    : 254 ( 44.3%)
Similarity (.)  : 211 ( 36.8%)

Fig. 14 (1)

Glyceraldehyde-3-phosphate dehydrogenase sequences of
Bacillus stearothermophilus (upper sequence) and
Rattus norvegicus (Rat) (lower sequence)

+++ Identical aminoacids: Bacillus / Rat (182 = 54.3%)

+ Similar, not identical aminoacids: Bacillus / Rat (115)

```
                    5                   10                  15
Ala Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn Val
    +++ +++ +++ +++  +  +++ +++ +++ +++ +++ +++ +++ +++      +++
 -  Val Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val
                       5                  10                  15

                20                  25                  30
Phe Arg Ala Ala Leu Lys Asn Pro Asp Ile Glu Val Val Ala Val Asn
    +++ +++ +++  +   +           +   +   +   +  +++ +++  +  +++
Thr Arg Ala Ala Phe Ser Cys Asp Lys Val Asp Ile Val Ala Ile Asn
                   20                  25                  30

                35                  40                  45
Asp  -  Leu Thr Asp Ala Asn Thr Leu Ala His Leu Leu Lys Tyr Asp
+++     +   +  +++  +  +++      +   +   +   +   +   +  +++ +++
Asp Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln Tyr Asp
                35                  40                  45

            50                  55                  60
Ser Val His Gly Arg Leu Asp Ala Glu Val Ser Val Asn Gly Asn Asn
+++  +  +++ +++  +   +   +   +   +  +++  +   +   +   +   +   +
Ser Thr His Gly Lys Phe Asn Gly Thr Val Lys Ala Glu Asn Gly Lys
            50                  55                  60

        65                  70                  75
Leu Val Val Asn Gly Lys Glu Ile Ile Val Lys Ala Glu Arg Asp Pro
+++ +++  +  +++ +++ +++      +++  +   +       +  +++ +++ +++ +++
Leu Val Ile Asn Gly Lys Pro Ile Thr Ile Phe Gln Glu Arg Asp Pro
        65                  70                  75

 80                  85                  90                  95
Glu Asn Leu Ala Trp Gly Glu Ile Gly Val Asp Ile Val Val Glu Ser
    +   +       +++ +++  +      +++  +   +       +++ +++ +++ +++
Val Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val Glu Ser
 80                  85                  90                  95

                100                 105                 110
Thr Gly Arg Phe Thr Lys Arg Glu Asp Ala Ala Lys His Leu Glu Ala
+++ +++      +++ +++  +   +  +++  +  +++  +      +++ +++  +   +
Thr Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu Lys Gly
                100                 105                 110
```

Fig. 14 (2)

```
                115                 120                 125
Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Lys Asn Glu Asp Ile
+++ +++ +++  +  +++ +++ +++ +++ +++ +++  +   +   +   +        +
Gly Ala Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met
                115                 120                 125

        130                 135                 140
Thr Ile Val Met Gly Val Asn Gln Asp Lys Tyr Asp Pro Lys Ala His
     +  +++ +++ +++ +++ +++  +   +  +++ +++ +++      +   +
 -  Phe Val Met Gly Val Asn His Glu Lys Tyr Asp  -  Asn Ser Leu
                130                 135                 140

    145                 150                 155
His Val Ile Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Phe
 +   +   +  +++ +++ +++ +++ +++ +++ +++ +++ +++ +++ +++ +++  +
Lys Ile Val Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu
                145                 150                 155

160                 165                 170                 175
Ala Lys Val Leu His Glu Gln Phe Gly Ile Val Arg Gly Met Met Thr
+++ +++ +++  +  +++  +   +  +++ +++ +++ +++      +++  +  +++ +++
Ala Lys Val Ile His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr
        160                 165                 170

                    180                 185                 190
Thr Val His Ser Tyr Thr Asn Asp Gln Arg Ile Leu Asp Leu Pro His
+++ +++ +++  +      +++  +   +  +++  +   +   +  +++      +++
Thr Val His Ala Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser
    175                 180                 185

                195                 200                 205
Lys Asp Leu Arg Arg  -  Ala Arg Ala Ala Ala Glu Ser Ile Ile Pro
     +  +++  +  +++      +  +++  +  +++ +++  +   +  +++ +++ +++
Gly Lys Leu Trp Arg Asp Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro
190                 195                 200                 205

                210                 215                 220
Thr Thr Thr Gly Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu
 +   +  +++ +++ +++ +++ +++ +++ +++  +      +++  +  +++ +++ +++
Ala Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu
                210                 215                 220

        225                 230                 235
Lys Gly Lys Leu Asn Gly Met Ala Met Arg Val Pro Thr Pro Asn Val
 +  +++ +++ +++  +  +++ +++ +++  +  +++ +++ +++ +++ +++ +++ +++
Asn Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Pro Asn Val
                225                 230                 235

    240                 245                 250
Ser Val Val Asp Leu Val Ala Glu Leu Glu Lys Glu Val Thr Val Glu
+++ +++ +++ +++ +++  +      +++ +++ +++      +   +       +
Ser Val Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp
        240                 245                 250
```

08/716,169

Fig. 14 (3)

```
255                 260                 265                 270
Glu Val Asn Ala Ala Leu Lys Ala Ala Ala Glu Gly Glu Leu Lys Gly
 +   +   +       +   +  +++  +  +++ +++ +++ +++     +++ +++ +++
Asp Ile Lys Lys Val Val Lys Gln Ala Ala Glu Gly Pro Leu Lys Gly
    255                 260                 265

                    275                 280                 285
Ile Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Arg Asp Tyr Asn Gly
+++ +++  +  +++  +  +++  +   +   +  +++ +++     +++  +  +++  +
Ile Leu Gly Tyr Thr Glu Asp Gln Val Val Ser Cys Asp Phe Asn Ser
270                 275                 280                 285

            290                 295                 300
Ser Thr Val Ser Ser Thr Ile Asp Ala Leu Ser Thr Met Val Ile Asp
 +   +      +++ +++ +++  +  +++ +++      +   +   +   +   +   +
Asn Ser His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn
            290                 295                 300

        305                 310                 315
Gly Lys Met Val Lys Val Val Ser Trp Tyr Asp Asn Glu Thr Gly Tyr
 +   +   +  +++ +++  +   +  +++ +++ +++ +++ +++ +++     +++ +++
Asp Asn Ile Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr Gly Tyr
        305                 310                 315

    320                 325                 330
Ser His Arg Val Val Asp Leu Ala Ala Tyr Ile Ala Ser Lys Gly
+++  +  +++ +++ +++ +++ +++     +++ +++  +  +++ +++ +++  +
Ser Asn Arg Val Val Asp Leu Met Ala Tyr Met Ala Ser Lys Glu
        320                 325                 330
```